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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/927,565

DATE: 01/15/2002
TIME: 09:58:29

Input Set : N:\Crf3\RULE60\09927565.raw
Output Set: N:\CRF3\01152002\I927565.raw

#2.

SEQUENCE LISTING

- 3 (1) GENERAL INFORMATION:
- 5 (i) APPLICANT: Lal, Preeti
6 Shah, Purvi
7 Corley, Neil C.
- 9 (ii) TITLE OF INVENTION: HUMAN PREPRONEUROTENSIN/NEUROMEDIN N
- 11 (iii) NUMBER OF SEQUENCES: 4
- 13 (iv) CORRESPONDENCE ADDRESS:
14 (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
15 (B) STREET: 3174 Porter Drive
16 (C) CITY: Palo Alto
17 (D) STATE: CA
18 (E) COUNTRY: USA
19 (F) ZIP: 94304
- 21 (v) COMPUTER READABLE FORM:
22 (A) MEDIUM TYPE: Diskette
23 (B) COMPUTER: IBM Compatible
24 (C) OPERATING SYSTEM: DOS
25 (D) SOFTWARE: FastSEQ for Windows Version 2.0
- 27 (vi) CURRENT APPLICATION DATA:
28 (A) APPLICATION NUMBER: US/09/927,565
29 (B) FILING DATE: 09-Aug-2001
30 (C) CLASSIFICATION:
32 (vii) PRIOR APPLICATION DATA:
33 (A) APPLICATION NUMBER: 09/002,114
34 (B) FILING DATE:
36 (viii) ATTORNEY/AGENT INFORMATION:
37 (A) NAME: Billings, Lucy J.
38 (B) REGISTRATION NUMBER: 36,749
39 (C) REFERENCE/DOCKET NUMBER: PF-0450 US
- 41 (ix) TELECOMMUNICATION INFORMATION:
42 (A) TELEPHONE: 650-855-0555
43 (B) TELEFAX: 650-845-4166
44 (C) TELEX:
- 47 (2) INFORMATION FOR SEQ ID NO: 1:
49 (i) SEQUENCE CHARACTERISTICS:
50 (A) LENGTH: 170 amino acids
51 (B) TYPE: amino acid
52 (C) STRANDEDNESS: single
53 (D) TOPOLOGY: linear
- 55 (vii) IMMEDIATE SOURCE:
56 (A) LIBRARY: PITUNOT03
57 (B) CLONE: 1760566
- 59 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
61 Met Met Ala Gly Met Lys Ile Gln Leu Val Cys Met Leu Leu Ala
62 1 5 10 15
63 Phe Ser Ser Trp Ser Leu Cys Ser Asp Ser Glu Glu Met Lys Ala

ENTERED

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64	20	25	30	
65	Leu Glu Ala Asp Phe Leu Thr Asn Met His Thr Ser Lys Ile Ser Lys			
66	35	40	45	
67	Ala His Val Pro Ser Trp Lys Met Thr Leu Leu Asn Val Cys Ser Leu			
68	50	55	60	
69	Val Asn Asn Leu Asn Ser Pro Ala Glu Glu Thr Gly Glu Val His Glu			
70	65	70	75	80
71	Glu Glu Leu Val Ala Arg Arg Lys Leu Pro Thr Ala Leu Asp Gly Phe			
72	85	90	95	
73	Ser Leu Glu Ala Met Leu Thr Ile Tyr Gln Leu His Lys Ile Cys His			
74	100	105	110	
75	Ser Arg Ala Phe Gln His Trp Glu Leu Ile Gln Glu Asp Ile Leu Asp			
76	115	120	125	
77	Thr Gly Asn Asp Lys Asn Gly Lys Glu Glu Val Ile Lys Arg Lys Ile			
78	130	135	140	
79	Pro Tyr Ile Leu Lys Arg Gln Leu Tyr Glu Asn Lys Pro Arg Arg Pro			
80	145	150	155	160
81	Tyr Ile Leu Lys Arg Asp Ser Tyr Tyr Tyr			
82	165	170		

84 (2) INFORMATION FOR SEQ ID NO: 2:

86 (i) SEQUENCE CHARACTERISTICS:

87 (A) LENGTH: 1351 base pairs
88 (B) TYPE: nucleic acid
89 (C) STRANDEDNESS: single
90 (D) TOPOLOGY: linear

93 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

95	NNCTAAAGCC AGCTGAAGGA AAGAGGAAGT GCTAGAGAGA GCCCCCTTCA GTGTGCTTCT	60
96	GACTTTACG GACTTGGCTT GTTAGAAGGC TGAAAGATGA TGGCAGGAAT GAAAATCCAG	120
97	CTTGTATGCA TGCTACTCCT GGCTTTCAGC TCCTGGAGTC TGTGCTCAGA TTCAGAAGAG	180
98	GAAATGAAAG CATTAGAAGC AGATTTCTTG ACCAATATGC ATACATCAAA GATTAGTAAA	240
99	GCACATGTC CCTCTGGAA GATGACTCTG CTAAATGTT GCAGTCTTGT AAATAATTG	300
100	AACAGCCCAG CTGAGGAAAC AGGAGAAGTT CATGAAGAGG AGCTTGTG AAGAAGGAAA	360
101	CTTCCTACTG CTTTAGATGG CTTTAGCTTGAAGCAATGT TGACAATATA CCAGCTCCAC	420
102	AAAATCTGTC ACAGCAGGGC TTTTCAACAC TGGGAGTTAA TCCAGGAAGA TATTCTTGAT	480
103	ACTGGAAATG ACAAAAATGG AAAGGAAGAA GTCATAAAGA GAAAAATTCC TTATATTCTG	540
104	AAACGGCAGC TGTATGAGAA TAAACCCAGA AGACCCTACA TACTCAAAAG AGATTCTTAC	600
105	TATTACTGAG AGAATAAATC ATTTATTAC ATGTGATTGT GATTCTACAT CCCTTAATT	660
106	AATATCAAAT TATATTGTG TGAAAATGTG ACAAAACACAC TTATCTGTCT CTTCTACAAT	720
107	TGTGGTTTAT TGAATGTGAT TTTTCTGCAC TAATATAAT TAGACTAAGT GTTTCAAAT	780
108	AAATCTAAAT CTTCAGCATG ATGTGTTGT TATAATTGGA GTAGATATTA ATTAAGTCAC	840
109	CTGTATAATG TTTGTAATT TTGCAAAACA TATCTTGAGT TGTTAAACA GTCAAAATGT	900
110	TTGATATTTC ATACCAGCTT ATGAGCTCAA AGTACTACAG CAAAGCTAG CCTGCATATC	960
111	ATTCACCCAA AACAAAGTAA TAGGCCTCT TTTATTATTT TGACTGAATG TTTTATGGAA	1020
112	TTGAAAGAAA CATACTTCT TTTCAAGACT TCCTCATGAA TCTCTCAATT ATAGGAAAAG	1080
113	TTATTGTGAT AAAATAGGAA CAGCTGAAAG ATTGATTAAT GAACTATTGT TATTACTTCC	1140
114	TATTTTAATG AATGACATTG AACTGGATT TTTGACCTGT TAATGGACTT GGTAGCTATT	1200
115	AGAAGGACAC TTGACCTCCA ATAGAAAAAA AATAAAGAAA TAAAAGAAG TATAAAAGTA	1260
116	ATAAAATAAA ATCAGAAGAG AAAAAGAAAA AGAAAAGTAA AAAGAGGGGG GACACACCAT	1320
117	AAGAACCAAT ACCCGGGAAT TTTCGGAGCG A	1351

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120 (2) INFORMATION FOR SEQ ID NO: 3:
122 (i) SEQUENCE CHARACTERISTICS:
123 (A) LENGTH: 169 amino acids
124 (B) TYPE: amino acid
125 (C) STRANDEDNESS: single
126 (D) TOPOLOGY: linear
128 (vii) IMMEDIATE SOURCE:
129 (A) LIBRARY: GenBank
130 (B) CLONE: 163424
132 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
134 Met Ala Gly Met Lys Ile Gln Leu Val Cys Met Ile Leu Leu Ala Phe
135 1 5 10 15
136 Ser Ser Trp Ser Leu Cys Ser Asp Ser Glu Glu Glu Met Lys Ala Leu
137 20 25 30
138 Glu Thr Asp Leu Leu Thr Asn Met His Thr Ser Lys Ile Ser Lys Ala
139 35 40 45
140 Ser Val Pro Ser Trp Lys Met Ser Leu Leu Asn Val Cys Ser Leu Ile
141 50 55 60
142 Asn Asn Leu Asn Ser Gln Ala Glu Glu Thr Gly Glu Phe His Glu Glu
143 65 70 75 80
144 Glu Leu Ile Thr Arg Arg Lys Phe Pro Ala Ala Leu Asp Gly Phe Ser
145 85 90 95
146 Leu Glu Ala Met Leu Thr Ile Tyr Gln Leu Gln Lys Ile Cys His Ser
147 100 105 110
148 Arg Ala Phe Gln His Trp Glu Leu Ile Gln Glu Asp Ile Leu Asp Ala
149 115 120 125
150 Gly Asn Asp Lys Asn Glu Lys Glu Glu Val Ile Lys Arg Lys Ile Pro
151 130 135 140
152 Tyr Ile Leu Lys Arg Gln Leu Tyr Glu Asn Lys Pro Arg Arg Pro Tyr
153 145 150 155 160
154 Ile Leu Lys Arg Gly Ser Tyr Tyr Tyr
155 165
157 (2) INFORMATION FOR SEQ ID NO: 4:
159 (i) SEQUENCE CHARACTERISTICS:
160 (A) LENGTH: 169 amino acids
161 (B) TYPE: amino acid
162 (C) STRANDEDNESS: single
163 (D) TOPOLOGY: linear
165 (vii) IMMEDIATE SOURCE:
166 (A) LIBRARY: GenBank
167 (B) CLONE: 92546
169 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
171 Met Ile Gly Met Asn Leu Gln Leu Val Cys Leu Thr Leu Leu Ala Phe
172 1 5 10 15
173 Ser Ser Trp Ser Leu Cys Ser Asp Ser Glu Glu Asp Val Arg Ala Leu
174 20 25 30
175 Glu Ala Asp Leu Leu Thr Asn Met His Ala Ser Lys Val Ser Lys Gly
176 35 40 45
177 Ser Pro Pro Ser Trp Lys Met Thr Leu Leu Asn Val Cys Ser Leu Ile

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178	50	55	60														
179	Asn	Asn	Leu	Asn	Ser	Ala	Ala	Glu	Glu	Ala	Gly	Glu	Met	Arg	Asp	Asp	
180	65		70					75						80			
181	Asp	Leu	Val	Ala	Lys	Arg	Lys	Leu	Pro	Leu	Val	Leu	Asp	Asp	Phe	Ser	
182					85						90				95		
183	Leu	Glu	Ala	Leu	Leu	Thr	Val	Phe	Gln	Leu	Gln	Lys	Ile	Cys	Arg	Ser	
184					100				105					110			
185	Arg	Ala	Phe	Gln	His	Trp	Glu	Ile	Ile	Gln	Glu	Asp	Ile	Leu	Asp	His	
186					115				120					125			
187	Gly	Asn	Glu	Lys	Thr	Glu	Lys	Glu	Glu	Val	Ile	Lys	Arg	Lys	Ile	Pro	
188					130				135					140			
189	Tyr	Ile	Leu	Lys	Arg	Gln	Leu	Tyr	Glu	Asn	Lys	Pro	Arg	Arg	Pro	Tyr	
190					145				150					155			160
191	Ile	Leu	Lys	Arg	Ala	Ser	Tyr	Tyr	Tyr								
192						165											

VERIFICATION SUMMARY

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L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]